



<223> Kex2 cleavage site

<400> 217

Glu Ala Glu Ala Glu Phe

1 5

<210> 218

<211> 387

<212> DNA

<213> Dermatophagoides pteronyssinus

<220>

<221> CDS

<222> (1)..(387)

<220>

<221> mutation

<222> (16)..(18)

<220>

<221> mutation

<222> (43)..(45)

<220>

<221> mutation

<222> (88)..(90)

<220>

<221> mutation

<222> (184)..(186)

<220>

<221> mutation

<222> (220)..(222)

<220>

<221> mutation

<222> (244)..(246)

<400> 218

gat caa gtc gat gtc gcc gat tgt gcc aac cat gaa atc aaa gaa gtt
Asp Gln Val Asp Val Ala Asp Cys Ala Asn His Glu Ile Lys Glu Val
1 5 10 15

48

ttg gta cca gga tgt cat ggt tca gaa cca tgt atc att aac cgt ggt
Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile Asn Arg Gly
20 25 30

96

aaa cca ttc caa ttg gaa gcc gtt ttc gaa gcc aac caa aac aca aaa
Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr Lys
35 40 45

144

acc gct aaa att gaa atc aaa gcc tca atc gat ggt tta tca gtt gat		192	
Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu Ser Val Asp			
50	55	60	
gtt ccc ggt atc gat cca aat gca tgc aat tac atg aaa tgc cca ttg		240	
Val Pro Gly Ile Asp Pro Asn Ala Cys Asn Tyr Met Lys Cys Pro Leu			
65	70	75	80
gtt aat gga caa caa tat gat att aaa tat aca tgg aat gtt ccg aaa		288	
Val Asn Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val Pro Lys			
85	90	95	
att gca cca aaa tct gaa aat gtt gtc gtc act gtt aaa gtt atg ggt		336	
Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met Gly			
100	105	110	
gat gat ggt gtt ttg gcc tgt gct att gca act cat gct aaa atc cgc		384	
Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile Arg			
115	120	125	
gat		387	
Asp			

<210> 219
<211> 129
<212> PRT
<213> Dermatophagoides pteronyssinus

<400> 219

Asp Gln Val Asp Val Ala Asp Cys Ala Asn His Glu Ile Lys Glu Val			
1	5	10	15

Leu Val Pro Gly Cys His Gly Ser Glu Pro Cys Ile Ile Asn Arg Gly		
20	25	30

Lys Pro Phe Gln Leu Glu Ala Val Phe Glu Ala Asn Gln Asn Thr Lys		
35	40	45

Thr Ala Lys Ile Glu Ile Lys Ala Ser Ile Asp Gly Leu Ser Val Asp		
50	55	60

Val Pro Gly Ile Asp Pro Asn Ala Cys Asn Tyr Met Lys Cys Pro Leu			
65	70	75	80

Val Asn Gly Gln Gln Tyr Asp Ile Lys Tyr Thr Trp Asn Val Pro Lys		
85	90	95

Ile Ala Pro Lys Ser Glu Asn Val Val Val Thr Val Lys Val Met Gly
100 105 110

Asp Asp Gly Val Leu Ala Cys Ala Ile Ala Thr His Ala Lys Ile Arg
115 120 125

Asp